Fig 1a kappa light chain

Atom	type					X	Y	Z	Occ	B	
ATOM	928	N	GLN	L	124	-44.718	27.024	79.393	1.00	37.64	N
ATOM	929	CA	GLN	L	124	-43.847	25.897	79.535	1.00	38.32	C
ATOM	930	C	GLN	L	124	-44.309	25.088	80.734	1.00	39.17	C
ATOM	931	O	GLN	L	124	-44.458	23.876	80.578	1.00	40.06	O
ATOM	932	CB	GLN	L	124	-42.414	26.311	79.745	1.00	37.76	C
ATOM	933	CG	GLN	L	124	-41.615	25.026	79.581	1.00	34.56	C
ATOM	934	CD	GLN	L	124	-40.133	25.152	79.698	1.00	34.95	C
ATOM	935	OE1	GLN	L	124	-39.440	24.138	79.682	1.00	34.80	O
ATOM	936	NE2	GLN	L	124	-39.569	26.344	79.820	1.00	39.75	N
ATOM	954	N	SER	L	127	-46.898	22.499	80.067	1.00	50.58	N
ATOM	955	CA	SER	L	127	-46.559	21.169	79.588	1.00	49.80	C
ATOM	956	C	SER	L	127	-45.890	20.274	80.637	1.00	49.81	C
ATOM	957	O	SER	L	127	-45.283	19.248	80.318	1.00	50.44	O
ATOM	958	CB	SER	L	127	-45.674	21.333	78.368	1.00	50.26	C
ATOM	959	OG	SER	L	127	-44.618	22.263	78.551	1.00	51.43	O
ATOM	960	N	GLY	L	128	-45.954	20.623	81.919	1.00	48.65	N
ATOM	961	CA	GLY	L	128	-45.371	19.786	82.925	1.00	47.11	C
ATOM	962	C	GLY	L	128	-43.851	19.873	82.985	1.00	46.88	C
ATOM	963	O	GLY	L	128	-43.322	19.013	83.700	1.00	46.88	O
ATOM	964	N	THR	L	129	-43.091	20.805	82.358	1.00	46.66	N
ATOM	965	CA	THR	L	129	-41.625	20.919	82.516	1.00	43.85	C
ATOM	966	C	THR	L	129	-41.246	22.341	82.832	1.00	37.58	C
ATOM	967	O	THR	L	129	-42.031	23.269	82.637	1.00	35.77	O
ATOM	968	CB	THR	L	129	-40.785	20.528	81.250	1.00	48.03	C
ATOM	969	OG1	THR	L	129	-41.566	20.726	80.058	1.00	54.58	O
ATOM	970	CG2	THR	L	129	-40.269	19.111	81.408	1.00	49.23	C
ATOM	976	N	SER	L	131	-37.741	24.856	82.399	1.00	29.71	N
ATOM	977	CA	SER	L	131	-36.337	25.100	82.108	1.00	27.40	C
ATOM	978	C	SER	L	131	-35.958	26.455	82.672	1.00	24.38	C
ATOM	979	O	SER	L	131	-36.663	27.454	82.446	1.00	23.59	O
ATOM	980	CB	SER	L	131	-36.097	25.078	80.593	1.00	29.26	C
ATOM	981	OG	SER	L	131	-36.672	23.985	79.880	1.00	28.43	O
ATOM	989	N	VAL	L	133	-32.859	29.248	82.770	1.00	23.53	N
ATOM	990	CA	VAL	L	133	-31.671	29.552	81.985	1.00	21.58	C
ATOM	991	C	VAL	L	133	-30.829	30.592	82.700	1.00	21.93	C
ATOM	992	O	VAL	L	133	-31.363	31.514	83.297	1.00	22.42	O
ATOM	993	CB	VAL	L	133	-32.042	30.112	80.607	1.00	21.06	C
ATOM	994	CG1	VAL	L	133	-30.831	30.026	79.693	1.00	25.56	C
ATOM	995	CG2	VAL	L	133	-33.149	29.296	79.958	1.00	24.10	C
ATOM	1188	N	GLY	L	157	-26.853	18.788	90.054	1.00	53.00	N
ATOM	1189	CA	GLY	L	157	-26.116	18.154	88.943	1.00	52.14	C
ATOM	1190	C	GLY	L	157	-27.023	17.720	87.749	1.00	51.94	C
ATOM	1191	O	GLY	L	157	-26.809	16.631	87.208	1.00	52.06	O
ATOM	1192	N	ASN	L	158	-28.025	18.503	87.273	1.00	50.46	N
ATOM	1193	CA	ASN	L	158	-28.946	18.183	86.142	1.00	46.46	C
ATOM	1194	C	ASN	L	158	-29.116	19.347	85.106	1.00	44.90	C
ATOM	1195	O	ASN	L	158	-30.222	19.704	84.625	1.00	40.45	O
ATOM	1196	CB	ASN	L	158	-30.312	17.839	86.692	1.00	47.64	C
ATOM	1197	CG	ASN	L	158	-30.916	19.055	87.386	1.00	52.21	C
ATOM	1198	OD1	ASN	L	158	-30.438	19.529	88.430	1.00	47.79	O
ATOM	1199	ND2	ASN	L	158	-31.930	19.646	86.768	1.00	55.19	N
ATOM	1200	N	SER	L	159	-27.980	19.972	84.739	1.00	41.19	N
ATOM	1201	CA	SER	L	159	-27.943	21.083	83.811	1.00	38.82	C
ATOM	1202	C	SER	L	159	-27.136	20.769	82.554	1.00	38.54	C
ATOM	1203	O	SER	L	159	-26.262	19.891	82.610	1.00	39.32	O
ATOM	1204	CB	SER	L	159	-27.323	22.257	84.505	1.00	32.87	C
ATOM	1205	OG	SER	L	159	-26.007	21.915	84.912	1.00	34.12	O
ATOM	1206	N	GLN	L	160	-27.397	21.485	81.451	1.00	37.38	N
ATOM	1207	CA	GLN	L	160	-26.575	21.389	80.266	1.00	35.88	C
ATOM	1208	C	GLN	L	160	-26.118	22.789	79.886	1.00	32.74	C
ATOM	1209	O	GLN	L	160	-26.831	23.765	80.112	1.00	28.45	O
ATOM	1210	CB	GLN	L	160	-27.325	20.798	79.077	1.00	40.64	C
ATOM	1211	CG	GLN	L	160	-27.352	19.273	79.129	1.00	47.64	C
ATOM	1212	CD	GLN	L	160	-27.353	18.619	77.751	1.00	51.42	C
ATOM	1213	OE1	GLN	L	160	-26.474	17.841	77.354	1.00	54.61	O

Fig 1a kappa light chain

ATOM	1214	NE2	GLN	L	160	-28.351	18.941	76.956	1.00	51.87	N
ATOM	1215	N	GLU	L	161	-24.947	22.884	79.252	1.00	32.26	N
ATOM	1216	CA	GLU	L	161	-24.315	24.116	78.812	1.00	30.57	C
ATOM	1217	C	GLU	L	161	-24.096	24.228	77.315	1.00	29.51	C
ATOM	1218	O	GLU	L	161	-24.030	23.218	76.609	1.00	31.47	O
ATOM	1219	CB	GLU	L	161	-22.989	24.254	79.465	1.00	31.63	C
ATOM	1220	CG	GLU	L	161	-23.068	25.232	80.584	1.00	39.52	C
ATOM	1221	CD	GLU	L	161	-22.438	24.715	81.857	1.00	45.11	C
ATOM	1222	OE1	GLU	L	161	-21.196	24.764	81.949	1.00	43.57	O
ATOM	1223	OE2	GLU	L	161	-23.211	24.287	82.736	1.00	48.88	O
ATOM	1224	N	SER	L	162	-23.964	25.449	76.818	1.00	27.95	N
ATOM	1225	CA	SER	L	162	-23.733	25.712	75.415	1.00	24.52	C
ATOM	1226	C	SER	L	162	-22.917	27.003	75.355	1.00	23.12	C
ATOM	1227	O	SER	L	162	-23.213	27.968	76.057	1.00	21.32	O
ATOM	1228	CB	SER	L	162	-25.089	25.831	74.776	1.00	24.91	C
ATOM	1229	OG	SER	L	162	-24.944	26.008	73.380	1.00	28.23	O
ATOM	1332	N	SER	L	176	-24.700	29.533	78.016	1.00	20.73	N
ATOM	1333	CA	SER	L	176	-25.984	29.359	78.650	1.00	20.18	C
ATOM	1334	C	SER	L	176	-25.967	28.050	79.391	1.00	19.90	C
ATOM	1335	O	SER	L	176	-25.400	27.058	78.938	1.00	18.83	O
ATOM	1336	CB	SER	L	176	-27.081	29.343	77.602	1.00	22.81	C
ATOM	1337	OG	SER	L	176	-26.755	28.427	76.557	1.00	27.50	O
ATOM	1338	N	SER	L	177	-26.543	28.045	80.570	1.00	21.10	N
ATOM	1339	CA	SER	L	177	-26.716	26.843	81.325	1.00	22.83	C
ATOM	1340	C	SER	L	177	-28.233	26.701	81.427	1.00	24.50	C
ATOM	1341	O	SER	L	177	-28.927	27.679	81.752	1.00	26.47	O
ATOM	1342	CB	SER	L	177	-26.100	27.030	82.675	1.00	20.36	C
ATOM	1343	OG	SER	L	177	-25.923	25.738	83.209	1.00	25.00	O
ATOM	1344	N	THR	L	178	-28.783	25.535	81.113	1.00	26.21	N
ATOM	1345	CA	THR	L	178	-30.193	25.289	81.284	1.00	25.67	C
ATOM	1346	C	THR	L	178	-30.333	24.182	82.316	1.00	26.52	C
ATOM	1347	O	THR	L	178	-29.692	23.127	82.251	1.00	25.41	O
ATOM	1348	CB	THR	L	178	-30.797	24.854	79.993	1.00	24.43	C
ATOM	1349	OG1	THR	L	178	-30.504	25.890	79.065	1.00	27.73	O
ATOM	1350	CG2	THR	L	178	-32.288	24.606	80.101	1.00	23.92	C
ATOM	1359	N	THR	L	180	-33.064	21.776	83.928	1.00	33.72	N
ATOM	1360	CA	THR	L	180	-34.412	21.334	83.617	1.00	36.96	C
ATOM	1361	C	THR	L	180	-34.895	20.441	84.742	1.00	39.75	C
ATOM	1362	O	THR	L	180	-34.162	19.554	85.220	1.00	40.12	O
ATOM	1363	CB	THR	L	180	-34.439	20.578	82.248	1.00	37.34	C
ATOM	1364	OG1	THR	L	180	-34.262	21.580	81.236	1.00	38.56	O
ATOM	1365	CG2	THR	L	180	-35.746	19.829	81.975	1.00	36.31	C
ATOM	1366	N	LEU	L	181	-36.102	20.772	85.213	1.00	41.45	N
ATOM	1367	CA	LEU	L	181	-36.790	19.955	86.189	1.00	41.68	C
ATOM	1368	C	LEU	L	181	-38.283	19.907	85.844	1.00	41.64	C
ATOM	1369	O	LEU	L	181	-38.823	20.667	85.022	1.00	39.32	O
ATOM	1370	CB	LEU	L	181	-36.472	20.527	87.616	1.00	41.26	C
ATOM	1371	CG	LEU	L	181	-36.887	21.835	88.321	1.00	44.99	C
ATOM	1372	CD1	LEU	L	181	-35.940	21.997	89.487	1.00	42.76	C
ATOM	1373	CD2	LEU	L	181	-36.694	23.093	87.505	1.00	45.40	C

Fig 1b heavy chain

Atom type						X	Y	Z	Occ	B	
ATOM	2595	N	LYS	H	126	-39.678	16.046	64.413	1.00	20.92	N
ATOM	2596	CA	LYS	H	126	-40.480	16.635	65.460	1.00	19.79	C
ATOM	2597	C	LYS	H	126	-40.194	18.131	65.371	1.00	21.17	C
ATOM	2598	O	LYS	H	126	-39.025	18.554	65.306	1.00	23.97	O
ATOM	2599	CB	LYS	H	126	-40.054	16.081	66.825	1.00	18.88	C
ATOM	2600	CG	LYS	H	126	-41.090	16.590	67.794	1.00	26.44	C
ATOM	2601	CD	LYS	H	126	-40.944	16.341	69.291	1.00	32.32	C
ATOM	2602	CE	LYS	H	126	-41.916	17.243	70.134	1.00	37.31	C
ATOM	2603	NZ	LYS	H	126	-41.584	18.677	70.172	1.00	35.44	N
ATOM	2608	N	PRO	H	128	-40.310	22.204	66.796	1.00	18.58	N
ATOM	2609	CA	PRO	H	128	-39.950	22.699	68.117	1.00	19.70	C
ATOM	2610	C	PRO	H	128	-41.041	23.367	68.948	1.00	22.10	C
ATOM	2611	O	PRO	H	128	-42.127	23.691	68.475	1.00	25.30	O
ATOM	2612	CB	PRO	H	128	-38.769	23.602	67.812	1.00	18.78	C
ATOM	2613	CG	PRO	H	128	-39.053	24.200	66.457	1.00	17.91	C
ATOM	2614	CD	PRO	H	128	-39.898	23.122	65.749	1.00	20.81	C
ATOM	2615	N	SER	H	129	-40.828	23.620	70.221	1.00	24.82	N
ATOM	2616	CA	SER	H	129	-41.770	24.395	70.995	1.00	23.50	C
ATOM	2617	C	SER	H	129	-40.946	25.623	71.266	1.00	24.48	C
ATOM	2618	O	SER	H	129	-39.763	25.502	71.565	1.00	22.58	O
ATOM	2619	CB	SER	H	129	-42.105	23.686	72.286	1.00	28.31	C
ATOM	2620	OG	SER	H	129	-42.934	22.546	72.073	1.00	36.78	O
ATOM	2628	N	PHE	H	131	-40.521	28.925	73.626	1.00	30.04	N
ATOM	2629	CA	PHE	H	131	-41.040	29.482	74.848	1.00	27.87	C
ATOM	2630	C	PHE	H	131	-40.215	30.723	75.051	1.00	30.92	C
ATOM	2631	O	PHE	H	131	-39.007	30.683	74.789	1.00	26.23	O
ATOM	2632	CB	PHE	H	131	-40.810	28.570	76.022	1.00	30.11	C
ATOM	2633	CG	PHE	H	131	-41.537	27.235	75.970	1.00	30.98	C
ATOM	2634	CD1	PHE	H	131	-42.931	27.183	75.945	1.00	30.57	C
ATOM	2635	CD2	PHE	H	131	-40.808	26.050	75.966	1.00	33.12	C
ATOM	2636	CE1	PHE	H	131	-43.590	25.948	75.915	1.00	31.13	C
ATOM	2637	CE2	PHE	H	131	-41.479	24.815	75.932	1.00	33.57	C
ATOM	2638	CZ	PHE	H	131	-42.863	24.765	75.907	1.00	31.34	C
ATOM	2646	N	LEU	H	133	-38.146	33.716	77.032	1.00	38.18	N
ATOM	2647	CA	LEU	H	133	-37.285	33.930	78.190	1.00	34.16	C
ATOM	2648	C	LEU	H	133	-37.523	35.428	78.330	1.00	35.44	C
ATOM	2649	O	LEU	H	133	-37.005	36.294	77.609	1.00	32.35	O
ATOM	2650	CB	LEU	H	133	-35.823	33.622	77.863	1.00	29.24	C
ATOM	2651	CG	LEU	H	133	-35.533	32.258	77.309	1.00	22.14	C
ATOM	2652	CD1	LEU	H	133	-34.066	32.136	77.012	1.00	23.67	C
ATOM	2653	CD2	LEU	H	133	-35.970	31.213	78.300	1.00	27.77	C
ATOM	2749	N	LEU	H	150	-36.371	30.246	73.846	1.00	22.90	N
ATOM	2750	CA	LEU	H	150	-35.971	28.876	74.075	1.00	23.38	C
ATOM	2751	C	LEU	H	150	-36.705	28.058	73.003	1.00	25.45	C
ATOM	2752	O	LEU	H	150	-37.917	28.204	72.817	1.00	24.96	O
ATOM	2753	CB	LEU	H	150	-36.391	28.505	75.477	1.00	18.99	C
ATOM	2754	CG	LEU	H	150	-36.325	27.052	75.868	1.00	19.75	C
ATOM	2755	CD1	LEU	H	150	-34.917	26.528	75.789	1.00	22.45	C
ATOM	2756	CD2	LEU	H	150	-36.781	26.912	77.286	1.00	19.55	C
ATOM	2764	N	LYS	H	152	-37.287	24.376	72.183	1.00	25.67	N
ATOM	2765	CA	LYS	H	152	-37.209	23.103	72.858	1.00	23.11	C
ATOM	2766	C	LYS	H	152	-37.793	21.909	72.110	1.00	23.19	C
ATOM	2767	O	LYS	H	152	-38.886	21.985	71.563	1.00	22.11	O
ATOM	2768	CB	LYS	H	152	-37.905	23.319	74.200	1.00	25.76	C
ATOM	2769	CG	LYS	H	152	-37.302	22.378	75.195	1.00	29.14	C
ATOM	2770	CD	LYS	H	152	-37.759	22.579	76.622	1.00	30.74	C
ATOM	2771	CE	LYS	H	152	-36.922	21.597	77.460	1.00	28.69	C
ATOM	2772	NZ	LYS	H	152	-37.314	20.228	77.199	1.00	25.73	N
ATOM	2773	N	ASP	H	153	-37.045	20.807	72.047	1.00	25.81	N
ATOM	2774	CA	ASP	H	153	-37.461	19.487	71.575	1.00	22.60	C
ATOM	2775	C	ASP	H	153	-37.870	19.231	70.146	1.00	20.15	C
ATOM	2776	O	ASP	H	153	-38.939	18.761	69.803	1.00	18.56	O
ATOM	2777	CB	ASP	H	153	-38.561	19.010	72.523	1.00	26.65	C
ATOM	2778	CG	ASP	H	153	-38.083	18.807	73.962	1.00	26.68	C
ATOM	2779	OD1	ASP	H	153	-36.935	18.446	74.194	1.00	28.52	O

Fig 1b heavy chain

ATOM	2780	OD2	ASP	H	153	-38.866	19.018	74.873	1.00	26.88	O
ATOM	2940	N	PHE	H	175	-27.214	30.210	70.335	1.00	23.94	N
ATOM	2941	CA	PHE	H	175	-26.383	29.122	70.813	1.00	23.42	C
ATOM	2942	C	PHE	H	175	-26.478	27.831	69.986	1.00	23.74	C
ATOM	2943	O	PHE	H	175	-27.538	27.522	69.409	1.00	23.81	O
ATOM	2944	CB	PHE	H	175	-26.758	28.815	72.248	1.00	22.94	C
ATOM	2945	CG	PHE	H	175	-26.259	29.899	73.148	1.00	20.21	C
ATOM	2946	CD1	PHE	H	175	-24.971	29.801	73.645	1.00	19.49	C
ATOM	2947	CD2	PHE	H	175	-27.079	30.977	73.458	1.00	20.84	C
ATOM	2948	CE1	PHE	H	175	-24.497	30.807	74.468	1.00	20.36	C
ATOM	2949	CE2	PHE	H	175	-26.595	31.980	74.294	1.00	22.58	C
ATOM	2950	CZ	PHE	H	175	-25.300	31.901	74.800	1.00	21.02	C
ATOM	2951	N	PRO	H	176	-25.360	27.078	69.878	1.00	22.56	N
ATOM	2952	CA	PRO	H	176	-25.321	25.723	69.318	1.00	19.83	C
ATOM	2953	C	PRO	H	176	-26.377	24.835	69.977	1.00	21.20	C
ATOM	2954	O	PRO	H	176	-26.508	24.942	71.200	1.00	22.55	O
ATOM	2955	CB	PRO	H	176	-23.910	25.305	69.595	1.00	16.67	C
ATOM	2956	CG	PRO	H	176	-23.083	26.559	69.637	1.00	15.02	C
ATOM	2957	CD	PRO	H	176	-24.018	27.503	70.334	1.00	17.20	C
ATOM	2963	N	VAL	H	178	-28.150	21.582	71.822	1.00	22.66	N
ATOM	2964	CA	VAL	H	178	-27.623	20.460	72.565	1.00	21.24	C
ATOM	2965	C	VAL	H	178	-28.654	19.371	72.365	1.00	20.88	C
ATOM	2966	O	VAL	H	178	-29.868	19.553	72.269	1.00	22.54	O
ATOM	2967	CB	VAL	H	178	-27.441	20.749	74.109	1.00	23.34	C
ATOM	2968	CG1	VAL	H	178	-26.426	21.863	74.326	1.00	21.50	C
ATOM	2969	CG2	VAL	H	178	-28.744	21.171	74.737	1.00	25.02	C
ATOM	2970	N	LEU	H	179	-28.110	18.208	72.193	1.00	22.43	N
ATOM	2971	CA	LEU	H	179	-28.876	17.011	72.085	1.00	25.70	C
ATOM	2972	C	LEU	H	179	-29.097	16.527	73.522	1.00	25.97	C
ATOM	2973	O	LEU	H	179	-28.187	16.399	74.348	1.00	25.39	O
ATOM	2974	CB	LEU	H	179	-28.076	16.026	71.278	1.00	25.57	C
ATOM	2975	CG	LEU	H	179	-28.702	14.674	71.023	1.00	27.43	C
ATOM	2976	CD1	LEU	H	179	-29.897	14.757	70.074	1.00	19.28	C
ATOM	2977	CD2	LEU	H	179	-27.587	13.805	70.469	1.00	30.31	C
ATOM	2978	N	GLN	H	180	-30.365	16.320	73.815	1.00	27.28	N
ATOM	2979	CA	GLN	H	180	-30.821	15.886	75.111	1.00	25.86	C
ATOM	2980	C	GLN	H	180	-30.787	14.360	75.199	1.00	26.76	C
ATOM	2981	O	GLN	H	180	-30.630	13.675	74.180	1.00	27.19	O
ATOM	2982	CB	GLN	H	180	-32.233	16.463	75.292	1.00	28.23	C
ATOM	2983	CG	GLN	H	180	-32.316	17.984	75.105	1.00	28.44	C
ATOM	2984	CD	GLN	H	180	-33.725	18.562	75.115	1.00	31.65	C
ATOM	2985	OE1	GLN	H	180	-34.406	18.608	74.093	1.00	30.70	O
ATOM	2986	NE2	GLN	H	180	-34.230	19.012	76.261	1.00	30.98	N
ATOM	2987	N	SER	H	181	-30.940	13.753	76.391	1.00	28.39	N
ATOM	2988	CA	SER	H	181	-30.945	12.305	76.549	1.00	28.80	C
ATOM	2989	C	SER	H	181	-32.113	11.663	75.787	1.00	25.40	C
ATOM	2990	O	SER	H	181	-31.965	10.542	75.300	1.00	28.76	O
ATOM	2991	CB	SER	H	181	-30.979	12.001	78.067	1.00	31.94	C
ATOM	2992	OG	SER	H	181	-31.812	12.915	78.815	1.00	40.94	O
ATOM	2993	N	SER	H	182	-33.258	12.324	75.579	1.00	21.90	N
ATOM	2994	CA	SER	H	182	-34.325	11.787	74.720	1.00	24.38	C
ATOM	2995	C	SER	H	182	-33.959	11.687	73.227	1.00	25.28	C
ATOM	2996	O	SER	H	182	-34.562	10.902	72.497	1.00	29.85	O
ATOM	2997	CB	SER	H	182	-35.556	12.654	74.850	1.00	17.40	C
ATOM	2998	OG	SER	H	182	-35.104	13.995	74.772	1.00	19.22	O
ATOM	3003	N	LEU	H	184	-33.775	14.556	71.267	1.00	20.48	N
ATOM	3004	CA	LEU	H	184	-34.278	15.749	70.637	1.00	17.63	C
ATOM	3005	C	LEU	H	184	-33.314	16.869	71.000	1.00	18.68	C
ATOM	3006	O	LEU	H	184	-32.549	16.765	71.956	1.00	16.48	O
ATOM	3007	CB	LEU	H	184	-35.675	15.980	71.168	1.00	18.23	C
ATOM	3008	CG	LEU	H	184	-36.724	14.864	71.080	1.00	12.53	C
ATOM	3009	CD1	LEU	H	184	-37.909	15.249	71.922	1.00	10.58	C
ATOM	3010	CD2	LEU	H	184	-37.141	14.621	69.658	1.00	13.49	C
ATOM	3023	N	SER	H	186	-32.310	21.176	71.626	1.00	19.45	N
ATOM	3024	CA	SER	H	186	-32.755	22.411	72.223	1.00	20.48	C
ATOM	3025	C	SER	H	186	-31.701	23.450	71.937	1.00	23.05	C
ATOM	3026	O	SER	H	186	-30.521	23.102	71.874	1.00	25.18	O
ATOM	3027	CB	SER	H	186	-32.916	22.306	73.718	1.00	21.58	C

Fig 1b heavy chain

ATOM	3028	OG	SER	H	186	-34.253	21.920	74.021	1.00	32.73	O
ATOM	3029	N	LEU	H	187	-32.104	24.707	71.768	1.00	21.56	N
ATOM	3030	CA	LEU	H	187	-31.233	25.811	71.415	1.00	21.58	C
ATOM	3031	C	LEU	H	187	-31.765	27.082	72.120	1.00	23.47	C
ATOM	3032	O	LEU	H	187	-32.948	27.118	72.496	1.00	24.42	O
ATOM	3033	CB	LEU	H	187	-31.309	25.838	69.897	1.00	19.86	C
ATOM	3034	CG	LEU	H	187	-30.875	26.971	69.054	1.00	21.75	C
ATOM	3035	CD1	LEU	H	187	-30.413	26.485	67.691	1.00	19.38	C
ATOM	3036	CD2	LEU	H	187	-32.048	27.868	68.864	1.00	23.32	C
ATOM	3037	N	SER	H	188	-31.014	28.142	72.424	1.00	22.73	N
ATOM	3038	CA	SER	H	188	-31.587	29.401	72.873	1.00	21.20	C
ATOM	3039	C	SER	H	188	-31.069	30.509	71.988	1.00	20.80	C
ATOM	3040	O	SER	H	188	-29.961	30.400	71.441	1.00	21.00	O
ATOM	3041	CB	SER	H	188	-31.179	29.775	74.274	1.00	25.10	C
ATOM	3042	OG	SER	H	188	-31.586	28.721	75.127	1.00	31.30	O

Fig 2(a)

Human Fab constant light kappa alignment

```
                        1         1         1         1         1         1
                        0         1         2         3         4         5
                        3456789012345678901234567890123456789012345678901234567890123456789012
S02577_Ig_Kappa         ----------------VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
AAB50880_IgG1_Kappa     T-PLTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVBLLNNFYPREAKVQWKVDN
A23746_Ig_Kappa         S-PLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVGLLNNFYPREAKVQWKVDN
AAA58921_Ig_Kappa       ----------------TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
AAB86466_Ig_Kappa       W-FRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYHREAKVQWKVDN
AAA58922_Ig_Kappa       ----------------TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQRKVDN
223335_Ig_Kappa         F-PYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLDDFYPREAKVQWKVDN
CAA09181_Ig_Kappa       F-PFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
CAA09183_Ig_Kappa       YSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
                                ************************* **::** ****** ****

                        1         1         1         1         2         2
                        6         7         8         9         0         1
                        3456789012345678901234567890123456789012345678901234567890123456789012
S02577_Ig_Kappa         ALQSGNSQESVTZZDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
AAB50880_IgG1_Kappa     ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYABEVTHQGLSSPVTKSFNRGEB
A23746_Ig_Kappa         ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGEG
AAA58921_Ig_Kappa       ALQSGNSQESVTEQESKDSTYSLSSTLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGEC
AAB86466_Ig_Kappa       ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
AAA58922_Ig_Kappa       ALQSGNSQESVTEQESKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
223335_Ig_Kappa         ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
CAA09181_Ig_Kappa       ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
CAA09183_Ig_Kappa       ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE----------------------------
                        ************  :********************
```

Fig. 2(b)

Human Fab, heavy chain constant part alignment

```
                          1         1         1         1         1
                9         0         1         2         3         4
                901234567890123456789012345678901234567890123456789012345678
AAH06402_igg3   IELDIV---VVPAPMRGSLGFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
GC1_igg1        ------------------------------------ASTKGPSVFPLAPSSKSTSGGTAALG
A23511_igg3     ------------------------------------ASTKGPSVFPLAPCSRSTSGGTAALG
CAC20456_igg3   ------------------------------------ASFKGPSVFPLAPCSRSTPGGTAALG
CAA67886_igg3   -----------------------------------STKGPSVFPLAPCSRSTSGGTAALG
AAG00911_igg3   -----------------------------------FTKGPSVFPLAPCSRSTSGGTAALG
AAB59393_igg2   -----------------------------------STKGPSVFPLAPCSRSTSESTAALG
AAG00910_igg2   ----------IIYFDYADFIMDYWGQGTTVTVSTASTKGPSVFPLAPCSRSTSESTAALG
GC2_igg2        ------------------------------------ASTKGPSVFPLAPCSRSTSESTAALG
CAC20455_igg2   ------------------------------------ASFKGPSVFPLAPCSRSTSESTAALG
AAB59394_igg4   -----------------------------------STKGPSVFPLAPCSRSTSESTAALG
AAG00912_igg4   ----------IIYFDYADFIMDYWGQGTTVTVSTASTKGPSVFPLAPCSRSTSESTAALG
CAC20457_igg4   ------------------------------------ASFKGPSVFPLVPCSRSTSESTAALG
AAG00909_igg1   -----------------------------------STKGPSVFPLAPSSKSTSGGTAALG
229601_igg1     RDTAMF---FAHWG-----------QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
2ig2_H_igg1     GGHGFC---SS----ASCFGPDYWGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
1mco_H_igg1     ----------------VPLVVNPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
AAB28159_igg1K  --------------------FAYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLG
1aqk_H_igg      ---------VLFQQLVLYAPFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
8fab_H_igg1     -------RDYYDSGGYFTVAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
AAA70227_igg1   GAGVTLVRGAIKPSPDYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
2fb4_H_igg      G-------GHGFCSSASCFGPDYWGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
AAB50879_igg1   G----------------DVYNRQWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
AF184764_igg1   G----------------DVYNRQWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
AF184765_igg2   G----------------DVYNRQWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALG
1vge_H_igg1K    P------------YGGGKSEFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
A49444_igg1     LIAGG--------------IDVWGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
AAB24269_igg1   LIAGG--------------IDVWGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
AAA70228_igg3   ETMASR-----------KRAFDIWGQGTMVTVSAASTKGPSVFPLAPCSRSTSGGTAALG
                                                . ***:**.* * : . . .:**
```

Fig. 2(b)

```
                    1         1         1         1         1         2
                    5         6         7         8         9         0
                    901234567890123456789012345678901234567890123456789012345678
AAH06402_igg3       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
GC1_igg1            CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
A23511_igg3         CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVN
CAC20456_igg3       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVN
CAA67886_igg3       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVN
AAG00911_igg3       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVN
AAB59393_igg2       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD
AAG00910_igg2       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD
GC2_igg2            CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD
CAC20455_igg2       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD
AAB59394_igg4       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD
AAG00912_igg4       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQXSGLYSLSSVVTVPSSSLGTKTYTCNVD
CAC20457_igg4       CLVKDYFPEPVTVSWNSCALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD
AAG00909_igg1       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
229601_igg1         CLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
2ig2_H_igg1         CLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
1mco_H_igg1         CLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
AAB28159_igg1K      CLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS-DLYTLSSSVTVPSSTWPSETVTCNVA
1aqk_H_igg          CLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
8fab_H_igg1         CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
AAA70227_igg1       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
2fb4_H_igg          CLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
AAB50879_igg1       BLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIBNVN
AF184764_igg1       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
AF184765_igg2       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVD
1vge_H_igg1K        CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
A49444_igg1         CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
AAB24269_igg1       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
AAA70228_igg3       CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVSVPSSNLGTQTYTCNVN
                     ***.***:****:*** :*:**********  .**:*** *:****.  ::*   **
```

Fig. 2(b)

```
                    2         2         2         2         2         2
                    1         2         3         4         5         6
                    901234567890123456789012345678901234567890123456789012345678
AAH06402_igg3       HKPSNTKVDKKVEP----------------------------------------------
GC1_igg1            HKPSNTKVDKKVEP----------------------------------------------
A23511_igg3         HKPSNTKVDKRVEL------KTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPP
CAC20456_igg3       HKPSNTKVDKRVEL------KTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPP
CAA67886_igg3       HKPSNTKVDKRVEL------KTPLGDTTHTCPRCPEPK----------------------
AAG00911_igg3       HKPSNTKVDKRVEL------KTPLGDTPPPCPRCPEPK----------------------
AAB59393_igg2       HKPSNTKVDKTVER------KCCV------------------------------------
AAG00910_igg2       HKPSNTKVDKTVER------KCCV------------------------------------
GC2_igg2            HKPSNTKVDKTVER------KCCV------------------------------------
CAC20455_igg2       HKPSNTKVDKTVER------KCCV------------------------------------
AAB59394_igg4       HKPSNTKVDKRVES------KYGP------------------------------------
AAG00912_igg4       HKPSNTKVDKRVES------KYGP------------------------------------
CAC20457_igg4       HKPSNTKVDKRVES------KYGP------------------------------------
AAG00909_igg1       HKPSNTKVDKRVEPKSCDKT----------------------------------------
229601_igg1         HKPSNTKVDKKVEP----------------------------------------------
2ig2_H_igg1         HKPSNTKVDKRVEP----------------------------------------------
1mco_H_igg1         HKPSNTKVDKRVAP----------------------------------------------
AAB28159_igg1K      HPASSTKVDKKIVP----------------------------------------------
1aqk_H_igg          HKPSNTKVDKKVEP----------------------------------------------
8fab_H_igg1         HKPSNTKVDKKVEP----------------------------------------------
AAA70227_igg1       HKPSNTKVDKRVEP----------------------------------------------
2fb4_H_igg          HKPSNTKVDKRVEP----------------------------------------------
AAB50879_igg1       HKPSNTK-----------------------------------------------------
AF184764_igg1       HKPSNTKVDKRVEP----------------------------------------------
AF184765_igg2       HKPSNTKVDKTVER----------------------------------------------
1vge_H_igg1K        HKPSNTKVDKKVEP----------------------------------------------
A49444_igg1         HKPSNTKVDKKVEP----------------------------------------------
AAB24269_igg1       HKPSNTKVDKKVEP----------------------------------------------
AAA70228_igg3       HKPSNTKVDKTVEL----------------------------------------------
                    * .*.**
```

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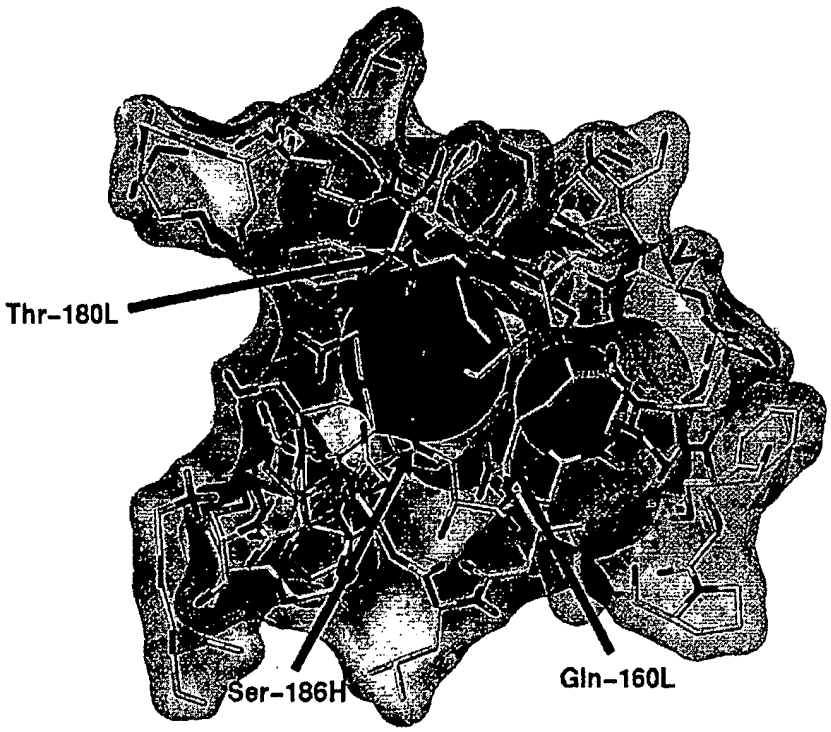
Figure 3



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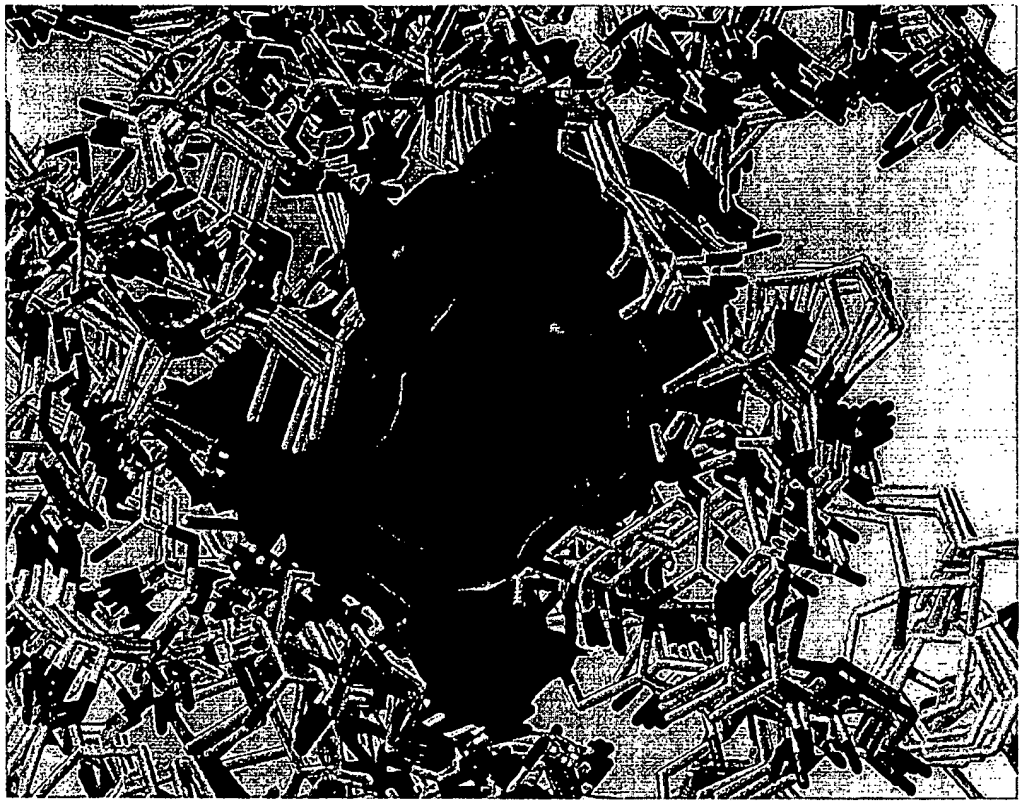
Figure 4